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Identification and Characterization of Glutathione S-transferase (*PgGST*) gene related to abiotic stress from *Panax ginseng*

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Plants have versatile detoxification systems to counter the phytotoxicity of a wide range of natural and synthetic compounds, which are present in the environment. Recently, many roles of glutathione S-transferase (GST) giving stress tolerance have been demonstrated. Expression of GSTs in plants is highly responsive to biotic and abiotic stress and to a wide variety of stress-associated chemicals. But little is known about the role of GSTs in ginseng plant. Antioxidant action of Korean ginseng (*Panax ginseng* C. A. Meyer) has been known as one of the pharmacological efficacies, so antioxidant enzymes in ginseng were thought to be important. Therefore, we aim to provide further information on the GST gene present in *P. ginseng* genome, as well as, its expression and functions. A GST cDNA (*PgGST*) was isolated from *Panax ginseng* by cDNA library construction, and its expression was investigated in relation to abiotic stresses. The cDNA was 1021 necleotides long and had an open reading frame of 753 bp with a deduced amino acid sequence of 251 residues. Its sequence shares high degrees of homologies with a number of other GSTs. To analyze the gene expression of *PgGST* gene against the oxidative and heavy metal stresses, we employed the quantitive RT-PCR and realtime PCR. Our results reveal that *PgGST* is induced by Cd, UV and after exposure to low temperatures. In addition, a vector system (35S-35S-AMV-PgGST-Tnos) has been constructed and was mobilized into *Agrobacterium tumerfaciens* strain MP 90 using disarmed Ti-plasmid. *PgGST* gene were introduced into the binary vector pRD 400 and introduced to *Nicotina tabacum* cv. Xanthi. Kanamycin resistance assay showed that transgenes were stably inherited to next generation. Transgenic tobacco plants overexpressing *PgGST* were normal in growth. The integration of 35S promoter, NPT Ⅱ, NOS terminator and *PgGST* gene into transgenic plants was confirmed by polymerase chain reaction (PCR). Southern blot analysis revealed that a single copy of gene exists in the transgenic tobacco genome. To investigate the expression of *PgGST* against several heavy metal stresses, we treated the tobacco seedling with various heavy metals. Reverse transcriptase-polymerase chain reaction (RT-PCR) analysis revealed that the *PgGST* expression in transgenic seedlings was increased by heavy metal stresses.